

2009-11-22 0425-1257PUS1_ST25 (2)
SEQUENCE LISTING

<110> MACHIDA, Kazuhiro et al.
<120> DNA PARTICIPATING IN HYDROXYLATION OF MACROLIDE COMPOUND
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<140> US 10/577,655
<141> 2006-05-01
<150> JP 2003-396828
<151> 2003-11-27
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Asp	Ile	Asp	Lys	Asp	Arg	Cys	Ile	Gly	Ala	Gly	Gln	Cys	Ala	Leu	Ala	
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Tyr Gly Pro Leu Arg Asp Gly Arg Ser Leu Ser Arg Val Thr Leu Phe
 35 40 45

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Asp Gly Arg Glu Val Trp Met Val Thr Gly His Ala Thr Ala Arg Ala
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Leu Leu Ala Asp Pro Arg Leu Ser Thr Asp Arg Thr Leu Pro Gly Phe
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Pro Val Pro Thr Ala Arg Phe Ala Ala Val Arg Asp Arg Arg Val Ala
85 90 95

Leu Leu Gly Val Asp Asp Pro Val His Gln Thr Gln Arg Arg Met Met
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Ile Pro Ser Phe Thr Leu Lys Arg Ala Ala Gly Leu Arg Pro Thr Ile
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Gln Arg Thr Val Asp Gly Leu Leu Asp Ala Met Ile Glu Lys Gly Pro
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180 185 190

Gly Ala Arg Glu Arg Leu Glu Glu Tyr Leu Gly Gly Leu Ile Asp Asp
195 200 205

Lys Glu Arg Gln Ala Glu Pro Gly Asp Gly Val Leu Asp Asp Leu Val
210 215 220

His Gln Arg Leu Arg Thr Gly Glu Leu Asp Arg Arg Asp Val Val Ala
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Ile Ser Leu Gly Thr Tyr Thr Leu Leu Arg His Pro Gly Arg Leu Ala
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Glu Leu Arg Ala Asp Pro Ala Leu Leu Pro Ala Ala Val Glu Glu Leu
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290 295 300

Asp Ile Glu Ile Ala Gly Ala Thr Ile Arg Ala Gly Glu Gly Val Leu
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Phe Ser Thr Ser Leu Ile Asn Arg Asp Glu Ser Val Phe Asp Asp Pro
325 330 335

Asp Thr Leu Asp Phe His Arg Ser Thr Arg His His Val Ala Phe Gly
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Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala Glu Leu
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Glu Ile Ala Leu Gly Thr Leu Leu Glu Arg Leu Pro Gly Leu Arg Leu
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Val Thr Glu Ala Ile Pro Tyr Phe Gln Asn Arg Thr Cys Pro Tyr His							
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Pro Pro Ala Ala Tyr Gln Pro Leu Arg Gly Ala Gly Pro Leu Ser His							
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Val Thr Phe Tyr Asp Gly Arg Lys Val Trp Ala Val Thr Gly His Pro							
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Glu Ala Arg Ala Leu Leu Thr Asp Gln Arg Leu Ser Ala Asp Arg Gln							
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Asn Pro Ala Phe Pro Val Pro Phe Glu Arg Phe Ala Ala Ile Arg Arg							
65 70 75 80							
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Val Arg Thr Pro Leu Ile Gly Val Asp Asp Pro Glu His Asn Thr Gln							
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Arg Arg Met Leu Ile Pro Ser Phe Ser Leu Lys Arg Thr Ala Ala Leu							
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Asp Gln Gly Pro Pro Thr Glu Leu Val Ser Ala Phe Ala Leu Pro Val							
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Val Thr Glu Ala Ile Pro Tyr Phe Gln Asn Arg Thr Cys Pro Tyr His
1 5 10 15

Pro Pro Ala Ala Tyr Gln Pro Leu Arg Gly Ala Gly Pro Leu Ser His
20 25 30

Val Thr Phe Tyr Asp Gly Arg Lys Val Trp Ala Val Thr Gly His Pro
35 40 45

Glu Ala Arg Ala Leu Leu Thr Asp Gln Arg Leu Ser Ala Asp Arg Gln
50 55 60

Asn Pro Ala Phe Pro Val Pro Phe Glu Arg Phe Ala Ala Ile Arg Arg
65 70 75 80

Val Arg Thr Pro Leu Ile Gly Val Asp Asp Pro Glu His Asn Thr Gln
85 90 95

Arg Arg Met Leu Ile Pro Ser Phe Ser Leu Lys Arg Thr Ala Ala Leu
 100 105 110

Arg Pro Glu Ile Gln Arg Ile Val Asp Gly Leu Leu Asp Arg Met Leu
 115 120 125

Asp Gln Gly Pro Pro Thr Glu Leu Val Ser Ala Phe Ala Leu Pro Val
 130 135 140

Pro Ser Met Val Ile Cys Ala Leu Leu Gly Val Ser Tyr Ala Asp His
 145 150 155 160

Glu Phe Phe Glu Glu Glu Ser Arg Arg Ile Leu Arg Gly Arg Ser Ala
 165 170 175

Glu Glu Ala Glu Asp Ala Arg Leu Lys Leu Glu Glu Tyr Phe Thr Gly
 180 185 190

Leu Ile Ala Ala Lys Glu Lys Asn Pro Gly Asp Gly Leu Leu Asp Glu
 195 200 205

Leu Ile Glu Asp Arg Leu Arg Thr Gly Ala Leu Thr Arg Asp Glu Leu
 210 215 220

Val Arg Leu Ala Met Ile Leu Leu Val Ala Gly His Glu Thr Thr Ala
 225 230 235 240

Asn Met Ile Ser Leu Gly Thr Phe Thr Leu Leu Asp His Pro Glu Gln
 245 250 255

Leu Ala Gln Leu Lys Ala Asp Glu Gly Leu Met Pro Ala Ala Ile Glu
 260 265 270

Glu Leu Leu Arg Phe Leu Ser Ile Ala Asp Gly Leu Leu Arg Val Ala
 275 280 285

Thr Glu Asp Ile Glu Ile Gly Gly Gln Val Ile Arg Ala Asp Asp Ala
 290 295 300

Val Leu Phe Pro Ala Ser Leu Ile Asn Arg Asp Glu Ala Ala Tyr Pro
 305 310 315 320

Ala Pro Asp Glu Leu Asp Leu Gly Arg Ser Ala Arg His His Val Ala
 325 330 335

ser Gly Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala
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340

345

350

Glu Met Glu Ile Ala Leu Arg Ser Leu Phe Thr Arg Ile Pro Gln Leu
 355 360 365

Arg Leu Ala Val Pro Ala Ala Glu Ile Pro Phe Lys Asp Gly Asp Thr
 370 375 380

Leu Gln Gly Met Ile Glu Leu Pro Leu Ala Trp
 385 390 395

<210> 6

<211> 64

<212> PRT

<213> Streptomyces sp.

<400> 6

Met Arg Ile Ala Ile Asp Thr Asp Arg Cys Ile Gly Ala Gly Gln Cys
 1 5 10 15

Ala Leu Thr Ala Pro Gly Gly Phe Thr Gln Asp Asp Asp Gly Phe Ser
 20 25 30

Ala Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Leu Val Arg
 35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile Ala Val Thr Asp Asp
 50 55 60

<210> 7

<211> 1860

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Sequence: nucleotide sequence with coding region derived from an unknown source

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<221> CDS

<222> (172)..(1383)

<220>

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<222> (1399)..(1593)

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ccagccagat ccgcagagta gccgatctgg ccgaacttga tgctgtgcac tggatgcctc 120

gggcatctaa tgaagatcgg cagcagcat ccttcgtctg cgaggtctcc c atg aca 177
 Met Thr

gac Asp	acg Thr	aca Thr 5	gac Asp	ctg Leu	acc Thr	gag Glu 10	ctg Leu	tca Ser	gat Asp	ccc Pro	gtc Val 15	tcc Ser 15	ttc Phe	ccc Pro	cag Gln	225
gac Asp	cgg Arg 20	agc Ser	tgc Cys	ccc Pro	tac Tyr	cac His 25	ccg Pro	ccc Pro	acc Thr	ggg Gly	tac Tyr 30	gac Asp	ccg Pro	ctg Leu	cgc Arg	273
acc Thr 35	gaa Glu	cgg Arg	ccg Pro	ccc Pro	gcc Ala 40	cgc Arg	atc Ile	cgg Arg	ctc Leu	tac Tyr 45	gac Asp	ggc Gly	cgc Arg	ccc Pro	gcc Ala 50	321
tgg Trp	ctc Leu	gtc Val	acc Thr	ggc Gly 55	cac His	gcc Ala	gtc Val	gcc Ala	cgt Arg 60	gac Asp	ctg Leu	ctg Leu	gtc Val	gac Asp 65	ccc Pro	369
cgc Arg	ctg Leu	tcc Ser	acg Thr 70	gac Asp	cgc Arg	acc Thr	cgc Arg	tgc Ser 75	ggc Gly	ttc Phe	ccg Pro	gcc Ala	aca Thr 80	act Thr	ccc Pro	417
cgc Arg	ttc Phe	gcc Ala 85	gcg Ala	gtc Val	cgc Arg	gac Asp	cgc Arg 90	aag Lys	ccg Pro	gcg Ala	ctc Leu	ctc Leu 95	ggc Gly	gtc Val	gac Asp	465
gac Asp	ccc Pro 100	aag Lys	cac His	cgc Arg	acc Thr	cag Gln 105	cgg Arg	tgg Trp	atg Met	atg Met	atc Ile 110	ccg Pro	agc Ser	ttc Phe	acc Thr	513
ctc Leu 115	agg Arg	cgc Arg	gcc Ala	acc Thr	gag Glu 120	ctc Leu	agg Arg	ccg Pro	cgc Arg	atc Ile 125	cag Gln	gag Glu	atc Ile	gtc Val	gac Asp 130	561
gaa Glu	ctg Leu	ctg Leu	gac Asp	gtg Val 135	atg Met	atc Ile	gcc Ala	cag Gln	gga Gly 140	ccc Pro	ccg Pro	gcc Ala	gac Asp	ctg Leu 145	gtg Val	609
cgt Arg	tcc Ser	ttc Phe	gcg Ala 150	ctg Leu	ccg Pro	gtg Val	ccg Pro	tcc Ser 155	atg Met	gtg Val	atc Ile	tgc Cys	gcc Ala 160	ctg Leu	ctc Leu	657
ggc Gly	gtg Val	ccc Pro 165	tac Tyr	gcc Ala	gac Asp	cac His	gag Glu 170	ttc Phe	ttc Phe	gag Glu	gac Asp	cag Gln 175	tcc Ser	agg Arg	cgg Arg	705
ctg Leu 180	ctg Leu	cgc Arg	gga Gly	ccg Pro	gcg Ala	gcc Ala 185	gag Glu	gac Asp	acg Thr	cag Gln	gac Asp 190	gcc Ala	ccg Arg	gac Asp	cgg Arg	753
ctc Leu 195	gcc Ala	gcg Ala	tac Tyr	ctg Leu	gag Glu 200	gac Asp	ctg Leu	atc Ile	gac Asp	gag Glu 205	aag Lys	cgg Arg	cgc Arg	cgg Arg	ccc Pro 210	801
ggg Gly	gac Asp	ggc Gly	ctg Leu	ctg Leu 215	gac Asp	gaa Glu	ctc Leu	gtc Val	cag Gln 220	cag Gln	cgt Arg	ctg Leu	aac Asn	gaa Glu 225	ggc Gly	849
gag Glu	ctc Leu	gac Asp	cgg Arg 230	gag Glu	gaa Glu	ctg Leu	acc Thr	gcg Ala 235	ctg Leu	gcg Ala	atg Met	atc Ile	ctg Leu 240	ctg Leu	gtc Val	897
gcg	ggc	cac	gag	acc	acc	gcc	aac	atg	atc	tcc	ctg	ggc	acc	tac	acg	945

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Ala Gly His Glu Thr Thr	Ala Asn Met Ile Ser Leu Gly Thr Tyr Thr	
245	250	255
ctc ctg ctg cac ccc gaa cgg ctg acc gag ctg cgc gcc gac ccc gcg		993
Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp Pro Ala		
260	265	270
ctg ctg ccg gcc gcc gtc gag gaa ctg atg cgg atg ctg tcc atc gcg		1041
Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser Ile Ala		
275	280	285
gac gga ctg ctg cgg cag gcc acc gag gac atc gag atc gcc ggg acc		1089
Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala Gly Thr		
295	300	305
acc atc agg gcc ggg gac ggc gtc gtc ttc tcc acc tct gtc atc aac		1137
Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val Ile Asn		
310	315	320
cgc gac gag gac gtc tac ccg gcc ccc gac acc ctc gac ttc cac cgc		1185
Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe His Arg		
325	330	335
tcg acc cgc cac cac gtc gcc ttc ggt ttc gga atc cac cag tgc ctc		1233
Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln Cys Leu		
340	345	350
ggc cag aac ctc gcc cgc acc gaa ctg gag atc gcc ctg cgc acg ctc		1281
Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg Thr Leu		
355	360	365
ctc gaa cgg ctg ccc acg ctc cgg ctc gcc gcc cca ccg gag gaa atc		1329
Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu Glu Ile		
375	380	385
ccc ttc aaa ccc ggc gac acc atc cag ggg atg ctg gaa ctc ccc gtc		1377
Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu Pro Val		
390	395	400
agc tgg taagaggctg ccgtc atg cat atc gag atc gac aag gac cgc tgc		1428
Ser Trp Met His Ile Glu Ile Asp Lys Asp Arg Cys		
405	410	
atc ggc gcc gga cag tgc gcc ctg acc gcc ccg ggt gtc ttc acc cag		1476
Ile Gly Ala Gly Gln Cys Ala Leu Thr Ala Pro Gly Val Phe Thr Gln		
415	420	425
gac gac gac ggc ttc agt gac ctg ttg ccc ggc cgg gag gac ggc gcc		1524
Asp Asp Asp Gly Phe Ser Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala		
435	440	445
ggc gac ccg atg gtc cgg gag gcc gcc agg gcc tgc ccc gtc agt gcc		1572
Gly Asp Pro Met Val Arg Glu Ala Ala Arg Ala Cys Pro Val Ser Ala		
450	455	460
atc acg ctg tcc gag gac ggg tagggggccg agccgcgccg cccgccggtc		1623
Ile Thr Leu Ser Glu Asp Gly		
465		
cgctgccgcg gcgccgtgcc gacgcggcgg ccggccggcc cgtccggtgc ccgtcgcgtc		1683
gccccgtggc cccggcgggc gctgattgac taggggttccc gggtgagcga acaggcccag		1743

aagccctccg gggcgccgcc cgcgaaagac accgggacgg cgcccgggaa accccttcct 1803
 ctacgtcgtc gtctgcgccg ccggcatcgc cgaaggcgtc agcaagctga tcaccgc 1860

<210> 8
 <211> 404
 <212> PRT
 <213> Unknown

<220>
 <223> Derived from an unknown source

<400> 8

Met Thr Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe
 1 5 10 15

Pro Gln Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro
 20 25 30

Leu Arg Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg
 35 40 45

Pro Ala Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val
 50 55 60

Asp Pro Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr
 65 70 75 80

Thr Pro Arg Phe Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly
 85 90 95

Val Asp Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser
 100 105 110

Phe Thr Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile
 115 120 125

Val Asp Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp
 130 135 140

Leu Val Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala
 145 150 155 160

Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser
 165 170 175

Arg Arg Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg
 180 185 190

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Asp Arg Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg
195 200 205

Arg Pro Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn
210 215 220

Glu Gly Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu
225 230 235 240

Leu Val Ala Gly His Glu Thr Thr Ala Asn Met Ile Ser Leu Gly Thr
245 250 255

Tyr Thr Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp
260 265 270

Pro Ala Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser
275 280 285

Ile Ala Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala
290 295 300

Gly Thr Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val
305 310 315 320

Ile Asn Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe
325 330 335

His Arg Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln
340 345 350

Cys Leu Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg
355 360 365

Thr Leu Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu
370 375 380

Glu Ile Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu
385 390 395 400

Pro Val Ser Trp

<210> 9
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Derived from an unknown source

<400> 9

Met His Ile Glu Ile Asp Lys Asp Arg Cys Ile Gly Ala Gly Gln Cys
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Ala Leu Thr Ala Pro Gly Val Phe Thr Gln Asp Asp Asp Gly Phe Ser
20 25 30

Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Met Val Arg
35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Ser Ala Ile Thr Leu Ser Glu Asp
50 55 60

Gly
65

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5Dm-3F Primer

<400> 10
ttcgcsctsc csgtcccstc satggtsat

29

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5Dm-3R Primer

<400> 11
gttgatsays gasgtsgaga a

21

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 6PIN-2F Primer

<400> 12
gctgcgctg gccctggagg acatcgagat

30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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 <400> 13
 ctgttcctcg aagaactcgt ggtcggcgta 30

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-NdeF Primer
 <400> 14
 gcccccatat gacggaactg acggacatca 30

<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
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 <400> 15
 gggccactag tcagccggcc ggttcggtca 30

<210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-BglF Primer
 <400> 16
 cgcatagatc ttcacccgag cgggtgatca 30

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-BglR Primer
 <400> 17
 tcccagatc ttgaagggtcc gcgtcaccgt 30

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5D-1R Primer

<400> 18
aggtgccag cgagatcatg tt 22

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 7PIN-2F Primer

<400> 19
ccatgatcct gctggtggcc ggccatgaga 30

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 07-NdeF Primer

<400> 20
gccccatatg accgaagcca tcccctactt 30

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 07-SpeR Primer

<400> 21
gccactagt ctaatcgtcg gtgaccgcaa 30

<210> 22
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5Dm-2R Primer

<400> 22
ctggatsgtg tcscs ggyt t 21

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5PIN-2F Primer

<400> 23
cggaatccac cagtgccctcg gccagaacct 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : tpm-NdeF Primer

<400> 24
ggcccatat gacagacacg acagacctga 30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : tpm-SpeR Primer

<400> 25
gcgcgactag tccccctacc cgtcctcgga 30